



#2

OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/016,236

DATE: 03/27/2002

TIME: 10:39:22

Input Set : N:\Crf3\RULE60\10016236.raw

Output Set: N:\CRF3\03272002\J016236.raw

SEQUENCE LISTING

3 (1) GENERAL INFORMATION:

5 (i) APPLICANT: Ryals, John
6 Friedrich, Leslie
7 Uknnes, Scott
8 Molina, Antonio
9 Ruess, Wilhelm
10 Knauf-Beiter, Gertrude
11 Kung, Ruth
12 Kessmann, Helmut
13 Oostendorp, Michael

ENTERED

16 (ii) TITLE OF INVENTION: METHOD FOR PROTECTING PLANTS

18 (iii) NUMBER OF SEQUENCES: 32

20 (iv) CORRESPONDENCE ADDRESS:

21 (A) ADDRESSEE: Novartis Corporation
22 (B) STREET: 3054 Cornwallis Road
23 (C) CITY: Research Triangle Park
24 (D) STATE: North Carolina
25 (E) COUNTRY: USA
26 (F) ZIP: 27709

28 (v) COMPUTER READABLE FORM:

29 (A) MEDIUM TYPE: Floppy disk
30 (B) COMPUTER: IBM PC compatible
31 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
32 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

34 (vi) CURRENT APPLICATION DATA:

C--> 35 (A) APPLICATION NUMBER: US/10/016,236
C--> 36 (B) FILING DATE: 12-Dec-2001

37 (C) CLASSIFICATION:

77 (vii) PRIOR APPLICATION DATA:

40 (A) APPLICATION NUMBER: 08/996,685
41 (B) FILING DATE:

45 (A) APPLICATION NUMBER: US 08/761,543

46 (B) FILING DATE: 6-DEC-1996

49 (A) APPLICATION NUMBER: US 60/034,378

50 (B) FILING DATE: 27-DEC-1996

53 (A) APPLICATION NUMBER: US 60/034,379

54 (B) FILING DATE: 27-DEC-1996

57 (A) APPLICATION NUMBER: US 60/034,382

58 (B) FILING DATE: 27-DEC-1996

61 (A) APPLICATION NUMBER: US 60/034,730

62 (B) FILING DATE: 10-JAN-1997

65 (A) APPLICATION NUMBER: US 60/035,021

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66 (B) FILING DATE: 10-JAN-1997
69 (A) APPLICATION NUMBER: US 60/035,022
70 (B) FILING DATE: 10-JAN-1997
73 (A) APPLICATION NUMBER: US 60/035,024
74 (B) FILING DATE: 10-JAN-1997
78 (A) APPLICATION NUMBER: US 08/875,015
79 (B) FILING DATE: 16-JUL-1997
82 (viii) ATTORNEY/AGENT INFORMATION:
83 (A) NAME: Meigs, J. Timothy
84 (B) REGISTRATION NUMBER: 38,241
85 (C) REFERENCE/DOCKET NUMBER: PF/5-21215/P1/CGC1912
87 (ix) TELECOMMUNICATION INFORMATION:
88 (A) TELEPHONE: (919) 541-8587
89 (B) TELEFAX: (919) 541-8689
92 (2) INFORMATION FOR SEQ ID NO: 1:
94 (i) SEQUENCE CHARACTERISTICS:
95 (A) LENGTH: 5655 base pairs
96 (B) TYPE: nucleic acid
97 (C) STRANDEDNESS: single
98 (D) TOPOLOGY: linear
100 (iii) MOLECULE TYPE: DNA (genomic)
102 (iii) HYPOTHETICAL: NO
104 (iv) ANTI-SENSE: NO
107 (ix) FEATURE:
108 (A) NAME/KEY: exon
109 (B) LOCATION: 2787..3347
110 (D) OTHER INFORMATION: /product= "1st exon of NIM1"
112 (ix) FEATURE:
113 (A) NAME/KEY: exon
114 (B) LOCATION: 3427..4162
115 (D) OTHER INFORMATION: /product= "2nd exon of NIM1"
117 (ix) FEATURE:
118 (A) NAME/KEY: exon
119 (B) LOCATION: 4271..4474
120 (D) OTHER INFORMATION: /product= "3rd exon of NIM1"
122 (ix) FEATURE:
123 (A) NAME/KEY: exon
124 (B) LOCATION: 4586..4866
125 (D) OTHER INFORMATION: /product= "4th exon of NIM1"
127 (ix) FEATURE:
128 (A) NAME/KEY: CDS
129 (B) LOCATION: join(2787..3347, 3427..4162, 4271..4474, 4586..4866)
132 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
134 TGTGATGCAA GTCATGGGAT ATTGCTTGT GTTAAGTATA CAAAACCAC ACGTGGATAC 60
136 ATAGTCTTCA AACCAACCAAC TAAACAGTAT CAGGTCTAC CAAAGCCAGA AGTGAAGGGT 120
138 TGGGATATGT CATTGGGTTT AGCGGTAATC GGATTGAACC CTTTCCGGTA TAAAATACAA 180
140 AGGCCTTCGCG AGTCTCGGCG TATGTGTATG TCTCGGGGTA TCTACCACATT GAATCACAGA 240
142 ACTTTATGT GCGAAGTTT CGATTCTGAT TCGTTTACCT GGAAGAGATT AGAAAATTG 300
144 CGTCTACCAA AAACAGACAG ATTAATTCTT TCCAACCCGA TACAAGTTTC GGGGTTCTTG 360

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146	CATTGGATAT	CACGGAACAA	CAATGTGATC	CGGTTTTGTC	TCAAAACCGA	AACTTGGTCC	420
148	TTCTTCCATA	CTCCGAACTC	TGATGTTTC	TCAGGATTAG	TCAGATACGA	AGGGAAGCTA	480
150	GGTGCTATT	GTCAGTGGAC	AAACAAAGAT	CAAGAAGATG	TTCACGAGTT	ATGGGTTTA	540
152	AAGAGCAGTT	TTGAAAAGTC	GTGGGTTAAA	GTGAAAGATA	TTAAAAGCAT	TGGAGTAGAT	600
154	TTGATTACGT	GGACTCCAAG	CAACGACGTT	GTATTGTTTC	GTAGTAGTGA	TCGTGGTTGC	660
156	CTCTACAACA	AAAACGAGA	GAAGTTGAAT	TTAGTTATG	CAAAAAAAGA	GGGATCTGAT	720
158	TGTTCTTCG	TTTGTTC	GTGTTGTTCT	GATTACGAGA	GGGTTGATCT	GAACCGGAAGA	780
160	AGCAACGGGC	CGACACTTTA	AAAAAAAAT	AAAAAAAATG	GGCCGACAAA	TGCAAACGTA	840
162	GTTGACAAGG	ATCTCAAGTC	TCAAGTCTCA	ATTGGCTCGC	TCATTGTTGG	GCATAAAATAT	900
164	ATCTAGTGT	GTGTTAATTGT	TTTTTATAAG	GTAAAAAGGA	ATATTGAATT	TTGTTCTTA	960
166	GGTTTATGTA	ATAATACCAA	ACATTGTTT	ATGAATATTT	AATCTGATTT	TTTGGCTAGT	1020
168	TATTTTATTA	TATCAAGGGT	TCCTGTTAT	AGTTGAAAAC	AGTTACTGTA	TAGAAAATAG	1080
170	TGTCCCATT	TTCTCTCTTA	AATAATATAT	TAGTTAATAA	AAGATATTTT	AATATATTAG	1140
172	ATATAACATAA	TATCTAAAGC	AACACATATT	TAGACACAAAC	ACGTAATATC	TTACTATTGT	1200
174	TTACATATAT	TTATAGCTTA	CCAATATAAC	CCGTATCTAT	GTGTTATAAG	CTTTTATACA	1260
176	ATATATGTAC	GGTATGCTGT	CCACGTATAT	ATATTCTCCA	AAAAAAACGC	ATGGTACACA	1320
178	AAATTTATTA	AATATTGGC	AATTGGGTGT	TTATCTAAAG	TTTATCACAA	TATTTATCAA	1380
180	CTATAATAGA	TGGTAGAAGA	TAaaaaaaATT	ATATCAGATT	GATTCAATTA	AATTTATAA	1440
182	TATATCATT	TAaaaaaaATT	ATTAAAAGAA	AACTATTCA	TAaaaattttt	CAAAAGATAA	1500
184	TTAGTAAAT	TAATTAATAA	TGTGATGCTA	TTGAGTTATA	GAGAGTTATT	GTAATTTTAC	1560
186	TTAAAATCAT	ACAAATCTTA	TCCTAATTTA	ACTTATCATT	TAAGAAATAC	AAAAGTAAAA	1620
188	AACGCGGAAA	GCAATAATTT	ATTTACCTTA	TTATAACTCC	TATATAAAAGT	ACTCTGTTA	1680
190	TTCAACATAA	TCTTACGTTG	TTGTATTCTAT	AGGCATCTT	AACCTATCTT	TTCATTTCT	1740
192	GATCTCGATC	GTGTTGATC	CAACAAAATG	AGTCTACCGG	TGAGGAACCA	AGAGGTGATT	1800
194	ATGCAGATT	CTTCTCTTC	TCAGGTTCCA	GCAACATCGA	GTCCGGAAAA	CACCAATCAA	1860
196	GTGAAGGATG	AGCCAAATTT	GTGTTAGACGT	GTTATGAATT	TGCTTTACG	TCGTAGTTAT	1920
198	TGAAAAAGCT	GATTTATCGC	ATGATTCAAGA	ACGAGAAGTT	GAAGGCAAAAT	AACTAAAGAA	1980
200	GTCTTTATA	TGTATACAAT	AATTGTTTT	AAATCAAATC	CTAATTAAAAA	AAATATATT	2040
202	ATTATGACTT	TCATGTTTT	AATGTAATT	ATTCTATAT	CTATAATGAT	TTTGTGTGA	2100
204	AGAGCGTTT	CATTTGCTAT	AGAACAAAGGA	GAATAGTTCC	AGGAAATATT	CGACTTGATT	2160
206	TAATTATAGT	GTAAACATGC	TGAACACTGA	AAATTACTTT	TTCAATAAAC	AAAAAATATA	2220
208	ATATAACATTA	CAAAACATTAT	GTGAATAAAAG	CATGAAACTT	AATATACGTT	CCCTTTATCA	2280
210	TTTACTTCA	AAGAAAATAA	ACAGAAATGT	AACTTCACA	TGTAATCTA	ATTCTTAAAT	2340
212	TTAAAAAATA	ATATTATAT	ATTTATATGA	AAATAACGAA	CCGGATGAAA	AATAAATTTT	2400
214	ATATATTTAT	ATCATCTCCA	AATCTAGTT	GGTTCAGGGG	CTTACCGAAC	CGGATTGAAC	2460
216	TTCTCATATA	CAAAAATTAG	CAACACAAA	TGTCTCCGGT	ATAAAATACTA	ACATTTATAA	2520
218	CCCGAACCGG	TTTAGCTTCC	TGTTATATCT	TTTAAAAAA	GATCTCTGAC	AAAGATTCC	2580
220	TTCCTGGAAA	TTTACCGGTT	TTGGTGAAAT	GTAAACCGTG	GGACGAGGAT	GCTCTTCAT	2640
222	ATCTCACCAC	CACTCTCGTT	GAATTGACTT	GGCTCTGCTC	GTCAATGGTT	ATCTTCGATC	2700
224	TTAACCAAA	TCCAGTTGAT	AAGGTCTCTT	CGTTGATTAG	CAGAGATCTC	TTTAATTG	2760
226	GAATTTCAAT	TCATCGGAAC	CTGTTG	ATG GAC ACC ATT	GAT GGA TTC	GCC	2813
227			Met Asp Thr Thr Ile Asp Gly Phe Ala				
228			1	5			
230	GAT TCT TAT	GAA ATC AGC	AGC ACT AGT	TTC GTC GCT	ACC GAT AAC	ACC	2861
231	Asp Ser Tyr	Glu Ile Ser	Ser Thr Ser	Phe Val	Ala Thr	Asp Asn Thr	
232	10	15		20	25		
234	GAC TCC TCT ATT	GTT TAT CTG	GCC GCC GAA	CAA GTA CTC	ACC GGA	CCT	2909
235	Asp Ser Ser	Ile Val Tyr	Leu Ala Ala	Glu Gln Val	Leu Thr	Gly Pro	
236		30		35	40		

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238 GAT GTA TCT GCT CTG CAA TTG CTC TCC AAC AGC TTC GAA TCC GTC TTT	2957
239 Asp Val Ser Ala Leu Gln Leu Leu Ser Asn Ser Phe Glu Ser Val Phe	
240 45 50 55	
242 GAC TCG CCG GAT GAT TTC TAC AGC GAC GCT AAG CTT GTT CTC TCC GAC	3005
243 Asp Ser Pro Asp Asp Phe Tyr Ser Asp Ala Lys Leu Val Leu Ser Asp	
244 60 65 70	
246 GGC CGG GAA GTT TCT TTC CAC CGG TGC GTT TTG TCA GCG AGA AGC TCT	3053
247 Gly Arg Glu Val Ser Phe His Arg Cys Val Leu Ser Ala Arg Ser Ser	
248 75 80 85	
250 TTC TTC AAG AGC GCT TTA GCC GCC GCT AAG AAG GAG AAA GAC TCC AAC	3101
251 Phe Phe Lys Ser Ala Leu Ala Ala Lys Lys Glu Lys Asp Ser Asn	
252 90 95 100 105	
254 AAC ACC GCC GCC GTG AAG CTC GAG CTT AAG GAG ATT GCC AAG GAT TAC	3149
255 Asn Thr Ala Ala Val Lys Leu Glu Leu Lys Glu Ile Ala Lys Asp Tyr	
256 110 115 120	
258 GAA GTC GGT TTC GAT TCG GTT GTG ACT GTT TTG GCT TAT GTT TAC AGC	3197
259 Glu Val Gly Phe Asp Ser Val Val Thr Val Leu Ala Tyr Val Tyr Ser	
260 125 130 135	
262 AGC AGA GTG AGA CCG CCG CCT AAA GGA GTT TCT GAA TGC GCA GAC GAG	3245
263 Ser Arg Val Arg Pro Pro Pro Lys Gly Val Ser Glu Cys Ala Asp Glu	
264 140 145 150	
266 AAT TGC TGC CAC GTG GCT TGC CGG CCG GCG GTG GAT TTC ATG TTG GAG	3293
267 Asn Cys Cys His Val Ala Cys Arg Pro Ala Val Asp Phe Met Leu Glu	
268 155 160 165	
270 GTT CTC TAT TTG GCT TTC ATC TTC AAG ATC CCT GAA TTA ATT ACT CTC	3341
271 Val Leu Tyr Leu Ala Phe Ile Phe Lys Ile Pro Glu Leu Ile Thr Leu	
272 170 175 180 185	
274 TAT CAG GTAAAACACC ATCTGCATTA AGCTATGGTT ACACATTCA GAATATGTT	3397
275 Tyr Gln	
278 TTACTTGAGT ACTTGTATTT GTATTCAG AGG CAC TTA TTG GAC GTT GTA GAC	3450
279 Arg His Leu Leu Asp Val Val Asp	
280 190 195	
282 AAA GTT GTT ATA GAG GAC ACA TTG GTT ATA CTC AAG CTT GCT AAT ATA	3498
283 Lys Val Val Ile Glu Asp Thr Leu Val Ile Leu Lys Leu Ala Asn Ile	
284 200 205 210	
286 TGT GGT AAA GCT TGT ATG AAG CTA TTG GAT AGA TGT AAA GAG ATT ATT	3546
287 Cys Gly Lys Ala Cys Met Lys Leu Leu Asp Arg Cys Lys Glu Ile Ile	
288 215 220 225	
290 GTC AAG TCT AAT GTA GAT ATG GTT AGT CTT GAA AAG TCA TTG CCG GAA	3594
291 Val Lys Ser Asn Val Asp Met Val Ser Leu Glu Lys Ser Leu Pro Glu	
292 230 235 240	
294 GAG CTT GTT AAA GAG ATA ATT GAT AGA CGT AAA GAG CTT GGT TTG GAG	3642
295 Glu Leu Val Lys Glu Ile Ile Asp Arg Arg Lys Glu Leu Gly Leu Glu	
296 245 250 255	
298 GTA CCT AAA GTA AAG AAA CAT GTC TCG AAT GTA CAT AAG GCA CTT GAC	3690
299 Val Pro Lys Val Lys Lys His Val Ser Asn Val His Lys Ala Leu Asp	
300 260 265 270 275	
302 TCG GAT GAT ATT GAG TTA GTC AAG TTG CTT TTG AAA GAG GAT CAC ACC	3738
303 Ser Asp Asp Ile Glu Leu Val Lys Leu Leu Lys Glu Asp His Thr	

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304	280	285	290	
306 AAT CTA GAT GAT GCG TGT GCT CTT CAT TTC GCT GTT GCA TAT TGC AAT				3786
307 Asn Leu Asp Asp Ala Cys Ala Leu His Phe Ala Val Ala Tyr Cys Asn				
308 295	300	305		
310 GTG AAG ACC GCA ACA GAT CTT TTA AAA CTT GAT CTT GCC GAT GTC AAC				3834
311 Val Lys Thr Ala Thr Asp Leu Leu Lys Leu Asp Leu Ala Asp Val Asn				
312 310	315	320		
314 CAT AGG AAT CCG AGG GGA TAT ACG GTG CTT CAT GTT GCT GCG ATG CGG				3882
315 His Arg Asn Pro Arg Gly Tyr Thr Val Leu His Val Ala Ala Met Arg				
316 325	330	335		
318 AAG GAG CCA CAA TTG ATA CTA TCT CTA TTG GAA AAA GGT GCA AGT GCA				3930
319 Lys Glu Pro Gln Leu Ile Leu Ser Leu Leu Glu Lys Gly Ala Ser Ala				
320 340	345	350	355	
322 TCA GAA GCA ACT TTG GAA GGT AGA ACC GCA CTC ATG ATC GCA AAA CAA				3978
323 Ser Glu Ala Thr Leu Glu Gly Arg Thr Ala Leu Met Ile Ala Lys Gln				
324 360	365	370		
326 GCC ACT ATG GCG GTT GAA TGT AAT AAT ATC CCG GAG CAA TGC AAG CAT				4026
327 Ala Thr Met Ala Val Glu Cys Asn Asn Ile Pro Glu Gln Cys Lys His				
328 375	380	385		
330 TCT CTC AAA GGC CGA CTA TGT GTA GAA ATA CTA GAG CAA GAA GAC AAA				4074
331 Ser Leu Lys Gly Arg Leu Cys Val Glu Ile Leu Glu Gln Glu Asp Lys				
332 390	395	400		
334 CGA GAA CAA ATT CCT AGA GAT GTT CCT CCC TCT TTT GCA GTG GCG GCC				4122
335 Arg Glu Gln Ile Pro Arg Asp Val Pro Pro Ser Phe Ala Val Ala Ala				
336 405	410	415		
338 GAT GAA TTG AAG ATG ACG CTG CTC GAT CTT GAA AAT AGA G				4162
339 Asp Glu Leu Lys Met Thr Leu Leu Asp Leu Glu Asn Arg				
340 420	425	430		
342 GTATCTATCA AGTCTTATTCTT CTTATATGTT TGAATTAAAT TTATGTCTC TCTATTAGGA				4222
344 AACTGAGTGA ACTAATGATA ACTATTCTT GTGTCGTCCA CTGTTTAG TT GCA CTT				4278
345		Val Ala Leu		
346		435		
348 GCT CAA CGT CTT TTT CCA ACG GAA GCA CAA GCT GCA ATG GAG ATC GCC				4326
349 Ala Gln Arg Leu Phe Pro Thr Glu Ala Gln Ala Ala Met Glu Ile Ala				
350 440	445	450		
352 GAA ATG AAG GGA ACA TGT GAG TTC ATA GTG ACT AGC CTC GAG CCT GAC				4374
353 Glu Met Lys Gly Thr Cys Glu Phe Ile Val Thr Ser Leu Glu Pro Asp				
354 455	460	465		
356 CGT CTC ACT GGT ACG AAG AGA ACA TCA CCG GGT GTA AAG ATA GCA CCT				4422
357 Arg Leu Thr Gly Thr Lys Arg Thr Ser Pro Gly Val Lys Ile Ala Pro				
358 470	475	480		
360 TTC AGA ATC CTA GAA GAG CAT CAA AGT AGA CTA AAA GCG CTT TCT AAA				4470
361 Phe Arg Ile Leu Glu Glu His Gln Ser Arg Leu Lys Ala Leu Ser Lys				
362 485	490	495		
364 ACC G GTATGGATTC TCACCCACTT CATCGGACTC CTTATCACAA AAAACAAAAC				4524
365 Thr				
366 500				
368 TAAATGATCT TTAAACATGG TTTGTTACT TGCTGTCTGA CCTTGTTTT TTTATCATCA				4584
370 G TG GAA CTC GGG AAA CGA TTC TTC CCG CGC TGT TCG GCA GTG CTC				4629

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 03/27/2002
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:18; Xaa Pos.29,34

VERIFICATION SUMMARY
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Input Set : N:\Crf3\RULE60\10016236.raw
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L:35 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:36 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:555 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=3
L:631 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=4
L:707 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=5
L:1417 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:2159 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=17
L:2183 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=18
L:2195 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18 after pos.:16
L:2198 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18 after pos.:32
L:2207 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=19
L:2231 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=20
L:2252 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=21
L:2276 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=22
L:2297 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=23
L:2321 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=24